



PCT10

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/018,997

DATE: 05/21/2002
 TIME: 15:36:42

Input Set : A:\78883143.app
 Output Set: N:\CRF3\05212002\J018997.raw

ENTERED

3 <110> APPLICANT: FAIRWEATHER, NEIL FRASER
 4 SINHA, KATHARINE
 6 <120> TITLE OF INVENTION: TETANUS TOXIN POLYPEPTIDES
 8 <130> FILE REFERENCE: 078883-0143
 10 <140> CURRENT APPLICATION NUMBER: 10/018,997
 11 <141> CURRENT FILING DATE: 2001-12-26
 13 <150> PRIOR APPLICATION NUMBER: PCT/GB00/02428
 14 <151> PRIOR FILING DATE: 2000-06-23
 16 <150> PRIOR APPLICATION NUMBER: GB 9914861.1
 17 <151> PRIOR FILING DATE: 1999-06-25
 19 <160> NUMBER OF SEQ ID NOS: 27
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1315
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Clostridium tetani
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 30 1 5 10 15
 32 Asp Thr Ile Ile Met Met Glu Pro Pro Tyr Cys Lys Gly Leu Asp Ile
 33 20 25 30
 35 Tyr Tyr Lys Ala Phe Lys Ile Thr Asp Arg Ile Trp Ile Val Pro Glu
 36 35 40 45
 38 Arg Tyr Glu Phe Gly Thr Lys Pro Glu Asp Phe Asn Pro Pro Ser Ser
 39 50 55 60
 41 Leu Ile Glu Gly Ala Ser Glu Tyr Tyr Asp Pro Asn Tyr Leu Arg Thr
 42 65 70 75 80
 44 Asp Ser Asp Lys Asp Arg Phe Leu Gln Thr Met Val Lys Leu Phe Asn
 45 85 90 95
 47 Arg Ile Lys Asn Asn Val Ala Gly Glu Ala Leu Leu Asp Lys Ile Ile
 48 100 105 110
 50 Asn Ala Ile Pro Tyr Leu Gly Asn Ser Tyr Ser Leu Leu Asp Lys Phe
 51 115 120 125
 53 Asp Thr Asn Ser Asn Ser Val Ser Phe Asn Leu Leu Glu Gln Asp Pro
 54 130 135 140
 56 Ser Gly Ala Thr Thr Lys Ser Ala Met Leu Thr Asn Leu Ile Ile Phe
 57 145 150 155 160
 59 Gly Pro Gly Pro Val Leu Asn Lys Asn Glu Val Arg Gly Ile Val Leu
 60 165 170 175
 62 Arg Val Asp Asn Lys Asn Tyr Phe Pro Cys Arg Asp Gly Phe Gly Ser
 63 180 185 190
 65 Ile Met Gln Met Ala Phe Cys Pro Glu Tyr Val Pro Thr Phe Asp Asn
 66 195 200 205

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68 Val Ile Glu Asn Ile Thr Ser Leu Thr Ile Gly Lys Ser Lys Tyr Phe
69      210                      215                      220
71 Gln Asp Pro Ala Leu Leu Leu Met His Glu Leu Ile His Val Leu His
72 225                      230                      235                      240
74 Gly Leu Tyr Gly Met Gln Val Ser Ser His Glu Ile Ile Pro Ser Lys
75      245                      250                      255
77 Gln Glu Ile Tyr Met Gln His Thr Tyr Pro Ile Ser Ala Glu Glu Leu
78      260                      265                      270
80 Phe Thr Phe Gly Gly Gln Asp Ala Asn Leu Ile Ser Ile Asp Ile Lys
81      275                      280                      285
83 Asn Asp Leu Tyr Glu Lys Thr Leu Asn Asp Tyr Lys Ala Ile Ala Asn
84      290                      295                      300
86 Lys Leu Ser Gln Val Thr Ser Cys Asn Asp Pro Asn Ile Asp Ile Asp
87 305                      310                      315                      320
89 Ser Tyr Lys Gln Ile Tyr Gln Gln Lys Tyr Gln Phe Asp Lys Asp Ser
90      325                      330                      335
92 Asn Gly Gln Tyr Ile Val Asn Glu Asp Lys Phe Gln Ile Leu Tyr Asn
93      340                      345                      350
95 Ser Ile Met Tyr Gly Phe Thr Glu Ile Glu Leu Gly Lys Lys Phe Asn
96      355                      360                      365
98 Ile Lys Thr Arg Leu Ser Tyr Phe Ser Met Asn His Asp Pro Val Lys
99      370                      375                      380
101 Ile Pro Asn Leu Leu Asp Thr Ile Tyr Asn Asp Thr Glu Gly Phe
102 385                      390                      395                      400
104 Asn Ile Glu Ser Lys Asp Leu Lys Ser Glu Tyr Lys Gly Gln Asn Met
105      405                      410                      415
107 Arg Val Asn Thr Asn Ala Phe Arg Asn Val Asp Gly Ser Gly Leu Val
108      420                      425                      430
110 Ser Lys Leu Ile Gly Leu Cys Lys Lys Ile Ile Pro Pro Thr Asn Ile
111      435                      440                      445
113 Arg Glu Asn Leu Tyr Asn Arg Thr Ala Ser Leu Thr Asp Leu Gly Gly
114      450                      455                      460
116 Glu Leu Cys Ile Lys Ile Lys Asn Glu Asp Leu Thr Phe Ile Ala Glu
117 465                      470                      475                      480
119 Lys Asn Ser Phe Ser Glu Glu Pro Phe Gln Asp Glu Ile Val Ser Tyr
120      485                      490                      495
122 Asn Thr Lys Asn Lys Pro Leu Asn Phe Asn Tyr Ser Leu Asp Lys Ile
123      500                      505                      510
125 Ile Val Asp Tyr Asn Leu Gln Ser Lys Ile Thr Leu Pro Asn Asp Arg
126      515                      520                      525
128 Thr Thr Pro Val Thr Lys Gly Ile Pro Tyr Ala Pro Glu Tyr Lys Ser
129      530                      535                      540
131 Asn Ala Ala Ser Thr Ile Glu Ile His Asn Ile Asp Asp Asn Thr Ile
132 545                      550                      555                      560
134 Tyr Gln Tyr Leu Tyr Ala Gln Lys Ser Pro Thr Thr Leu Gln Arg Ile
135      565                      570                      575
137 Thr Met Thr Asn Ser Val Asp Asp Ala Leu Ile Asn Ser Thr Lys Ile
138      580                      585                      590
140 Tyr Ser Tyr Phe Pro Ser Val Ile Ser Lys Val Asn Gln Gly Ala Gln

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141	595	600	605
143 Gly Ile Leu Phe Leu Gln Trp Val Arg Asp Ile Ile Asp Asp Phe Thr			
144 610	615	620	
146 Asn Glu Ser Ser Gln Lys Thr Thr Ile Asp Lys Ile Ser Asp Val Ser			
147 625	630	635	640
149 Thr Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn Ile Val Lys Gln Gly			
150 645	650	655	
152 Tyr Glu Gly Asn Phe Ile Gly Ala Leu Glu Thr Thr Gly Val Val Leu			
153 660	665	670	
155 Leu Leu Glu Tyr Ile Pro Glu Ile Thr Leu Pro Val Ile Ala Ala Leu			
156 675	680	685	
158 Ser Ile Ala Glu Ser Ser Thr Gln Lys Glu Lys Ile Ile Lys Thr Ile			
159 690	695	700	
161 Asp Asn Phe Leu Glu Lys Arg Tyr Glu Lys Trp Ile Glu Val Tyr Lys			
162 705	710	715	720
164 Leu Val Lys Ala Lys Trp Leu Gly Thr Val Asn Thr Gln Phe Gln Lys			
165 725	730	735	
167 Arg Ser Tyr Gln Met Tyr Arg Ser Leu Glu Tyr Gln Val Asp Ala Ile			
168 740	745	750	
170 Lys Lys Ile Ile Asp Tyr Glu Tyr Lys Ile Tyr Ser Gly Pro Asp Lys			
171 755	760	765	
173 Glu Gln Ile Ala Asp Glu Ile Asn Asn Leu Lys Asn Lys Leu Glu Glu			
174 770	775	780	
176 Lys Ala Asn Lys Ala Met Ile Asn Ile Asn Ile Phe Met Arg Glu Ser			
177 785	790	795	800
179 Ser Arg Ser Phe Leu Val Asn Gln Met Ile Asn Glu Ala Lys Lys Gln			
180 805	810	815	
182 Leu Leu Glu Phe Asp Thr Gln Ser Lys Asn Ile Leu Met Gln Tyr Ile			
183 820	825	830	
185 Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Leu Lys Lys Leu Glu			
186 835	840	845	
188 Ser Lys Ile Asn Lys Val Phe Ser Thr Pro Ile Pro Phe Ser Tyr Ser			
189 850	855	860	
191 Lys Asn Leu Asp Cys Trp Val Asp Asn Glu Glu Asp Ile Asp Val Ile			
192 865	870	875	880
194 Leu Lys Lys Ser Thr Ile Leu Asn Leu Asp Ile Asn Asn Asp Ile Ile			
195 885	890	895	
197 Ser Asp Ile Ser Gly Phe Asn Ser Ser Val Ile Thr Tyr Pro Asp Ala			
198 900	905	910	
200 Gln Leu Val Pro Gly Ile Asn Gly Lys Ala Ile His Leu Val Asn Asn			
201 915	920	925	
203 Glu Ser Ser Glu Val Ile Val His Lys Ala Met Asp Ile Glu Tyr Asn			
204 930	935	940	
206 Asp Met Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys			
207 945	950	955	960
209 Val Ser Ala Ser His Leu Glu Gln Tyr Gly Thr Asn Glu Tyr Ser Ile			
210 965	970	975	
212 Ile Ser Ser Met Lys Lys His Ser Leu Ser Ile Gly Ser Gly Trp Ser			
213 980	985	990	

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215 Val Ser Leu Lys Gly Asn Asn Leu Ile Trp Thr Leu Lys Asp Ser Ala
216          995          1000          1005
218 Gly Glu Val Arg Gln Ile Thr Phe Arg Asp Leu Pro Asp Lys Phe Asn
219    1010          1015          1020
221 Ala Tyr Leu Ala Asn Lys Trp Val Phe Ile Thr Ile Thr Asn Asp Arg
222 1025          1030          1035          1040
224 Leu Ser Ser Ala Asn Leu Tyr Ile Asn Gly Val Leu Met Gly Ser Ala
225          1045          1050          1055
227 Glu Ile Thr Gly Leu Gly Ala Ile Arg Glu Asp Asn Asn Ile Thr Leu
228          1060          1065          1070
230 Lys Leu Asp Arg Cys Asn Asn Asn Asn Gln Tyr Val Ser Ile Asp Lys
231          1075          1080          1085
233 Phe Arg Ile Phe Cys Lys Ala Leu Asn Pro Lys Glu Ile Glu Lys Leu
234    1090          1095          1100
236 Tyr Thr Ser Tyr Leu Ser Ile Thr Phe Leu Arg Asp Phe Trp Gly Asn
237 1105          1110          1115          1120
239 Pro Leu Arg Tyr Asp Thr Glu Tyr Tyr Leu Ile Pro Val Ala Ser Ser
240          1125          1130          1135
242 Ser Lys Asp Val Gln Leu Lys Asn Ile Thr Asp Tyr Met Tyr Leu Thr
243          1140          1145          1150
245 Asn Ala Pro Ser Tyr Thr Asn Gly Lys Leu Asn Ile Tyr Tyr Arg Arg
246          1155          1160          1165
248 Leu Tyr Asn Gly Leu Lys Phe Ile Ile Lys Arg Tyr Thr Pro Asn Asn
249    1170          1175          1180
251 Glu Ile Asp Ser Phe Val Lys Ser Gly Asp Phe Ile Lys Leu Tyr Val
252 1185          1190          1195          1200
254 Ser Tyr Asn Asn Asn Glu His Ile Val Gly Tyr Pro Lys Asp Gly Asn
255          1205          1210          1215
257 Ala Phe Asn Asn Leu Asp Arg Ile Leu Arg Val Gly Tyr Asn Ala Pro
258          1220          1225          1230
260 Gly Ile Pro Leu Tyr Lys Lys Met Glu Ala Val Lys Leu Arg Asp Leu
261    1235          1240          1245
263 Lys Thr Tyr Ser Val Gln Leu Lys Leu Tyr Asp Asp Lys Asn Ala Ser
264    1250          1255          1260
266 Leu Gly Leu Val Gly Thr His Asn Gly Gln Ile Gly Asn Asp Pro Asn
267 1265          1270          1275          1280
269 Arg Asp Ile Leu Ile Ala Ser Asn Trp Tyr Phe Asn His Leu Lys Asp
270          1285          1290          1295
272 Lys Ile Leu Gly Cys Asp Trp Tyr Phe Val Pro Thr Asp Glu Gly Trp
273    1300          1305          1310
275 Thr Asn Asp
276    1315
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280 <211> LENGTH: 21
281 <212> TYPE: DNA
282 <213> ORGANISM: Artificial Sequence
284 <220> FEATURE:
285 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
286    oligonucleotide

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289 gagcatatga aaaaccttga t                                21
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294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
299     oligonucleotide
301 <400> SEQUENCE: 3
302 cggatcctta gtcgttggtc ca                                22
305 <210> SEQ ID NO: 4
306 <211> LENGTH: 34
307 <212> TYPE: DNA
308 <213> ORGANISM: Artificial Sequence
310 <220> FEATURE:
311 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
312     oligonucleotide
314 <400> SEQUENCE: 4
315 ggttgcgact ggtacttcta aggatccgaa ttcg                    34
318 <210> SEQ ID NO: 5
319 <211> LENGTH: 34
320 <212> TYPE: DNA
321 <213> ORGANISM: Artificial Sequence
323 <220> FEATURE:
324 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
325     oligonucleotide
327 <400> SEQUENCE: 5
328 ccaacgctga ccatgaagat tcctaggctt aagc                    34
331 <210> SEQ ID NO: 6
332 <211> LENGTH: 34
333 <212> TYPE: DNA
334 <213> ORGANISM: Artificial Sequence
336 <220> FEATURE:
337 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
338     oligonucleotide
340 <400> SEQUENCE: 6
341 gactggtact tcgttcggc tgatgaaggt tgga                    34
344 <210> SEQ ID NO: 7
345 <211> LENGTH: 34
346 <212> TYPE: DNA
347 <213> ORGANISM: Artificial Sequence
349 <220> FEATURE:
350 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
351     oligonucleotide
353 <400> SEQUENCE: 7
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357 <210> SEQ ID NO: 8
358 <211> LENGTH: 34

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VERIFICATION SUMMARY

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